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OM protein - protein search, using sw model

Run on: August 12, 2005, 15:00:58 ; Search time 73 Seconds

(without alignments)
328.481 Million cell updates/sec

Title: US-10-068-725-4_COPY_105_166

Perfect score: 315

Sequence: 1 ENKLSPVNLPELRQRSG.....SPALPGLKSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1980s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	315	100.0	166	2 AAW75785	Aaw75785 Human lym
2	315	100.0	166	5 AAE15494	Aae15494 Human TAC
3	315	100.0	246	6 ABP97720	Abp97720 Amino aci
4	315	100.0	246	8 ADK00762	Adk00762 Native hu
5	315	100.0	247	3 AAY93998	Aay93998 Human BR4
6	315	100.0	247	7 ABR61797	Abri61797 Human RYZ
7	315	100.0	265	4 AAE09244	Aae09244 Human TAC
8	315	100.0	266	6 ABP97723	Abp97723 Amino aci
9	315	100.0	293	2 AAW75783	Aaw75783 Human lym
10	315	100.0	293	3 AAB36312	Aab36312 Human neu
11	315	100.0	293	3 AAY94000	Aay94000 A transme
12	315	100.0	293	4 AAE09240	Aae09240 Human TAC
13	315	100.0	293	4 AAY71914	Aay71914 Human tum
14	315	100.0	293	5 AAO14130	Aao14130 Human tra
15	315	100.0	293	5 ABB81488	Abb81488 Human TAC
16	315	100.0	293	5 AAU99512	Aau99512 Human TAC
17	315	100.0	293	5 AAE28962	Aae28962 Human TAC
18	315	100.0	293	5 AAU75408	Aau75408 Tumour ne
19	315	100.0	293	5 AAU09900	Aau09900 Human AGP
20	315	100.0	293	5 AAE15493	Aae15493 Human tra
21	315	100.0	293	5 ABG71496	Abg71496 Human tum
22	315	100.0	293	6 AAE35211	Aae35211 Human TAC
23	315	100.0	293	6 ABP60551	Abp60551 Human tum
24	315	100.0	293	6 ABP97716	Abp97716 Amino aci
25	315	100.0	293	6 AAO29592	Aao29592 Human DIT

ALIGNMENTS

RESULT 1

AAW75785
ID AAW75785 standard; protein; 166 AA.

AC AAW75785;

DT 18-JAN-1999 (first entry)

DE Human lymphocyte surface receptor extracellular domain.

KW TAC1; transmembrane activator and CAML-interactor;

KW calcium signal-modulating cyclophilin ligand; human;

KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;

KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;

KW immunosuppressive; graft versus host disease; transplant rejection;

KW therapy; signal transduction.

OS Homo sapiens.

PN WO9839361-A1.

PD 11-SEP-1998.

PF 03-MAR-1998; 98WO-US004270.

PR 03-MAR-1997; 97US-00810572.

PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

PI Bram RJ, Von Bulow G;

DR WPI; 1998-506346/43.

DR N-PSDB; AAV57330.

XX New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host disease.

PS Claim 8; Page 73; 89pp; English.

XX This is the amino acid sequence of the N-terminal, i.e. the

extracellular, domain of novel human transmembrane activator and CAML-

interactor (TAC1) protein (see AAW75783). TAC1 is a lymphocyte receptor

protein that is involved in the calcium activation pathway. It is

normally present in B-lymphocytes, and to a much lesser extent in

immature T-lymphocytes, and can therefore be targetted to specifically

regulate B cell responses without affecting T cell activity. The

extracellular domain of TAC1 functions as a binding site for a ligand

CC that stimulates the activation of the cell by inducing the binding of the
 CC C-terminal portion (see AAW5784) of TACI to the N-terminal domain of
 CC CAML. A recombinant form of the extracellular portion of TACI acts as a
 CC dominant-negative or blocking agent and acts to suppress the immune
 CC system. It can be used to treat or prevent autoimmune disease, graft
 CC rejection or graft versus host disease. The extracellular region is also
 CC used in a claimed method for identifying a ligand for TACI, in which
 CC binding of a candidate molecule is determined by detecting cellular
 CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription
 CC factor, or of NF-AT dependent transcription
 XX

SQ Sequence 166 AA;

Query Match 100.0%; Score 315; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 5.1e-33;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 DB 105 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
 QY 61 ST 62
 DB 165 ST 166

* RESULT 2

AAEL15494
 ID AAE15494 standard; protein; 166 AA.

AC AAE15494;

DT 12-MAR-2002 (first entry)

XX Human TACI extracellular domain.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

PR 27-JUN-2000; 2000US-0214591P.

PR 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.

XX Claim 1; Fig 12A; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a

CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human TACI protein extracellular domain
 XX

SQ Sequence 166 AA;

Query Match 100.0%; Score 315; DB 5; Length 166;
 Best Local Similarity 100.0%; Pred. No. 5.1e-33;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 DB 105 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
 QY 61 ST 62
 DB 165 ST 166

RESULT 3

ABP97720
 ID ABP97720 standard; protein; 246 AA.

XX ABP97720;

XX 28-MAY-2003 (first entry)

XX Amino acid sequence of human TACI receptor.

XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
 KW TALL-1; April; systemic lupus erythematosus.

XX Homo sapiens.

XX WO2003014294-A2.

XX 20-FEB-2003.

XX 24-JUL-2002; 2002WO-US023487.

XX 03-AUG-2001; 2001US-0310114P.

PR 30-APR-2002; 2002US-0377171P.

XX (GETH) GENENTECH INC.

XX Dixit V, Grewal I, Ridgway J, Yan M;

XX WPI; 2003-256560/25.

DR N-PSDB; ABZ68874.

XX New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
 PT preparing a composition for treating systemic lupus erythematosus.

XX Disclosure; Fig 5B; 153pp; English.

XX The present sequence represents a human TACI polypeptide. The
 CC specification also describes BR3 polypeptides. TACI and BR3 are
 CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
 CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
 CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for

CC preparing a composition for treating systemic lupus erythematosus

SQ Sequence 246 AA;

Query Match 100.0%; Score 315; DB 6; Length 246;

Best Local Similarity 100.0%; Pred. No. 8.5e-33; Mismatches 0; Indels 0; Gaps 0;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPRLRRQSRGSEVNNDSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 DB 59 ENKLRSPVNLPPRLRRQSRGSEVNNDSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118

QY 61 ST 62

DB 119 ST 120

RESULT 4

ADK00762
 ID ADK00762 standard; protein; 246 AA.

XX AC ADK00762;

DT 06-MAY-2004 (first entry)

XX DE Native human TACIs.

XX KW CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;
 KW Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;
 KW Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;
 KW Antibacterial; antiparasitic; systemic lupus erythematosus;
 KW diabetes mellitus; AIDS.

XX OS Homo sapiens.

XX PN WO2004011611-A2.

XX PD 05-FEB-2004.

XX PF 25-JUL-2003; 2003WO-US023421.

XX PR 25-JUL-2002; 2002US-0398530P.

XX PA (GETH) GENENTECH INC.

XX PI Chuntharpai A, Grewal I, Kim KJ, Yan M;

XX WPI; 2004-143841/14.

XX DR N-PSDB; ADK00761.

XX PT New anti-TACI receptor monoclonal antibody, useful for diagnosing and
 PT treating pathological conditions associated with tumor necrosis factor,
 PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or
 PT psoriasis.

XX PS Disclosure; SEQ ID NO 14; 110pp; English.

XX CC The present invention relates to an isolated monoclonal antibody which
 CC binds to a transmembrane activator of and CAML interactor (TACI)
 CC receptor. The TACI antibodies are useful for modulating TALL-1 or TACI
 CC polypeptide biological activity in mammalian cells, or for diagnosing and
 CC treating pathological conditions associated with TNF and TNF receptor-
 CC related molecules, e.g. cancer or immune-related disease, such as
 CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,
 CC systemic vasculitis, diabetes mellitus, Crohn's disease,
 CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or
 CC infectious diseases including AIDS, hepatitis infection, bacterial
 CC infection, fungal infection, protozoal infection and parasitic infection.
 CC The present sequence represents native human TACIs.

XX SQ Sequence 246 AA;

Query Match 100.0%; Score 315; DB 8; Length 246;

Best Local Similarity 100.0%; Pred. No. 8.5e-33; Mismatches 0; Indels 0; Gaps 0;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPRLRRQSRGSEVNNDSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60

DB 59 ENKLRSPVNLPPRLRRQSRGSEVNNDSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118

QY 61 ST 62

DB 119 ST 120

RESULT 5

AAV93998

ID AAY93998 standard; protein; 247 AA.

XX AC AAY93998;

XX DT 20-OCT-2000 (first entry)

XX DE Human BR43x2, an isoform of the TACI receptor.

XX KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Domain 1..120

XX FT /note= "extracellular domain"

XX FT Region 25..58

XX FT /note= "cysteine-rich pseudo repeat"

XX FT Domain 121..133

XX FT /note= "transmembrane domain"

XX FT Domain 134..247

XX FT /note= "cytoplasmic domain"

XX PN WO2000040716-A2.

XX XX 13-JUL-2000.

XX XX 07-JAN-2000; 2000WO-US000396.

XX XX 07-JAN-1999; 99US-00226533.

XX XX (ZYMO) ZYMOGENETICS INC.

XX XX Gross JA, Xu W, Madden K, Yee DP;

XX XX WPI; 2000-452538/39.

XX XX N-PSDB; AAA58556.

XX PT Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX XX Claim 62; Page 145; 175pp; English.

XX CC The present sequence represents a human BR43x2 polypeptide, which is an
 CC isoform of the transmembrane activator and CAML-interactor (TACI)
 CC receptor. TACI is a tumour necrosis factor (TNF) receptor. The
 CC extracellular domains of BR43x2, TACI or BCMA (a related B cell protein)
 CC contain a cysteine rich domain, and are used for inhibiting ztnf4
 CC activity. Ztnf4 is a TNF ligand. They may also be used for inhibiting

CC BR43x2, TAC1 or BCMA receptor-ligand engagement associated with activated
 CC or resting B lymphocytes, effector T-cells, or with antibody production.
 CC The antibody production is associated with an autoimmune disease selected
 CC from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
 CC and rheumatoid arthritis. The tnfr4 activity and BR43x2, TAC1 or BCMA
 CC receptor-ligand engagement is associated with asthma, bronchitis,
 CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,
 CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
 CC light chain neuropathy, amyloidosis, moderating immune response,
 CC immunosuppression, graft rejection, graft versus host disease,
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
 CC pain, swelling, anaemia, or septic shock. BR43x2, TAC1, and BCMA
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol
 CC or renal emboli
 XX
 SQ Sequence 247 AA;
 Query Match 100.0%; Score 315; DB 3; Length 247;
 Best Local Similarity 100.0%; Pred. No. 8.6e-33;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 DB 59 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118
 QY 61 ST 62
 DB 119 ST 120
 RESULT 6
 ABR61797
 ID ABR61797 standard; protein; 247 AA.
 AC ABR61797;
 DT 12-SEP-2003 (first entry)
 DE Human RYZN polypeptide.
 DE RYZN; TNFRSF; tumour necrosis factor receptor; antiarteriosclerotic;
 KW type III transmembrane protein; antidiabetic; hypotensive; antilipemic;
 KW human.
 KW
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..113
 FT /note= "extracellular domain"
 FT Domain 114..136
 FT /note= "transmembrane domain"
 FT Domain 137..247
 FT /note= "intracellular domain"
 XX WO2003045421-A1.
 XX
 XX 05-JUN-2003.
 XX
 XX 03-OCT-2002; 2002WO-18004581.
 XX
 XX 28-NOV-2001; 2001US-0334152P.
 XX
 XX (GEST) GENSET SA.
 XX
 XX Dyalynas D, Scalia A, Lucas J, Briggs K;
 XX WPI; 2003-513616/48.
 DR N-PSDB; ACC84638.
 XX
 XX New agonists or antagonists of RYZN activity, useful for increasing or
 FT reducing body weight, for maintaining weight loss, and for preventing or
 PT treating an obesity-related disease or disorder, e.g. atherosclerosis or

PT diabetes.
 XX
 PS Example; Page 32-33; 37pp; English.
 XX
 CC The invention relates to an agonist or antagonist of RYZN activity. RYZN
 CC is a member of the Tumour Necrosis Factor Receptor Super Family (TNFRSF)
 CC and is a Type III transmembrane protein. The agonist or antagonist of
 CC RYZN activity, or compositions comprising them is useful for preventing
 CC or treating an obesity-related disease or disorder, such as insulin
 CC resistance, hyperlipidemia, atherosclerosis, diabetes, hypertension,
 CC syndrome X, and hyperuricemia. These may also be used to increase or
 CC reduce body weight, or maintain weight loss. The present sequence
 CC represents the human RYZN polypeptide
 XX
 SQ Sequence 247 AA;
 Query Match 100.0%; Score 315; DB 7; Length 247;
 Best Local Similarity 100.0%; Pred. No. 8.6e-33;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 DB 59 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118
 QY 61 ST 62
 DB 119 ST 120
 RESULT 7
 AAE09244
 ID AAE09244 standard; protein; 265 AA.
 XX
 AC AAE09244;
 XX
 DT 19-NOV-2001 (first entry)
 XX
 DE Human TAC1 splice variant protein.
 XX
 KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 KW TAC1; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
 XX
 OS Homo sapiens.
 XX
 XX WO200160397-A1.
 XX
 XX 23-AUG-2001.
 XX
 XX 28-NOV-2000; 2000WO-US032378.
 XX
 XX 16-FEB-2000; 2000US-0182938P.
 XX
 XX 22-AUG-2000; 2000US-0226986P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 XX Yan M;
 XX WPI; 2001-541628/60.
 XX
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 XX activity, for treating autoimmune disorders and cancer, comprises
 XX exposing the cells to TALL-1 or APRIL polypeptide agonists or
 XX antagonists.
 XX
 XX Example 1; Fig 6; 160pp; English.
 PS
 XX
 XX The invention relates to methods of using one or more agonists or
 XX antagonists to modulate the activity of the members of TNF (tumour
 XX necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
 XX TAC1 or BCMA. The method is useful for treating pathological conditions
 XX or diseases associated with increased TALL-1 and APRIL expression or

CC activity. TALL-1 and APRIL antagonists are used to block the interaction
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
 CC present sequence is human TACI splice variant protein
 XX
 SQ Sequence 265 AA;

Query Match 100.0%; Score 315; DB 4; Length 265;
 Best Local Similarity 100.0%; Pred. No. 9.4e-33;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSGVEVNNDSNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 DB 105 ENKLSPVNLPPELRRQSGVEVNNDSNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
 DB 165 ST 166

RESULT 8
 ABP97723
 ID ABP97723 standard; protein; 266 AA.

XX ABP97723;

AC ABP97723;

DT 28-MAY-2003 (first entry)

XX Amino acid sequence of an alternatively spliced human TACI receptor.

DE Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
 KW TALL-1; April; systemic lupus erythematosus.
 XX Homo sapiens.

OS WO2003014294-A2.

PN 20-FEB-2003.

PD 24-JUL-2002; 2002WO-US023487.

PP 03-AUG-2001; 2001US-0310114P.

PR 30-APR-2002; 2002US-0377171P.

XX (GETH) GENENTECH INC.

XX Dixit V, Grewal I, Ridgway J, Yan M;

XX WPI; 2003-256560/25.

XX New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
 PT preparing a composition for treating systemic lupus erythematosus.

XX Disclosure; Fig 8; 153pp; English.

XX The present sequence represents an alternatively spliced human TACI
 CC polypeptide. The specification also describes BR3 polypeptides. TACI and
 CC BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and
 CC April bind to the TACI receptor, while TNF family ligands TALL-1 also
 CC binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful
 CC for preparing a composition for treating systemic lupus erythematosus

XX Sequence 266 AA;

Query Match 100.0%; Score 315; DB 6; Length 266;

Best Local Similarity 100.0%; Pred. No. 9.4e-33;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSGVEVNNDSNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 DB 105 ENKLSPVNLPPELRRQSGVEVNNDSNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
 DB 165 ST 166

RESULT 9
 AAW75783
 ID AAW75783 standard; protein; 293 AA.

XX AAW75783;

DT 18-JAN-1999 (first entry)

XX Human lymphocyte surface receptor TACI.

XX TACI; transmembrane activator and CAML-interactor;
 KW calcium signal-modulating cyclophilin ligand; human;
 KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;
 KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;
 KW immunosuppressive; graft versus host disease; transplant rejection;
 KW therapy.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..166 /label= Extracellular_domain

FT Peptide 34..71 /note= "Claim 8"

FT Domain 167..186 /note= "TNFR_NGFR motif"

FT Domain 187..294 /label= Transmembrane_domain

FT Domain 197..294 /label= Cytoplasmic_domain

XX WO9839361-A1.

XX 11-SEP-1998.

XX 03-MAR-1998; 98WO-US004270.

XX 03-MAR-1997; 97US-00810572.

XX (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX Bram RJ, Von Bulow G;

XX WPI; 1998-506346/43.

XX N-PSDB; AAV57328.

XX New isolated transmembrane activator protein - used to develop products
 PT for treating e.g. infections, cancers, autoimmune and inflammatory
 PT conditions, transplant rejection or graft-versus-host disease.

XX Claim 20; Fig 2a; 89pp; English.

XX This is the amino acid sequence of novel human transmembrane activator
 CC and CAML-interactor (TACI) protein, a lymphocyte receptor protein that is
 CC involved in the calcium activation pathway. TACI is normally present in B
 CC lymphocytes, and to a much lesser extent in immature T-lymphocytes, and
 CC can therefore be targeted to specifically regulate B cell responses
 CC without affecting T cell activity. TACI cDNA (seev57328) was isolated
 CC from a B-lymphocyte cDNA library using a yeast two-hybrid assay. Also
 CC claimed are the C-terminal (see AAW75784) and N-terminal (see AAW75785)
 CC fragments of TACI, recombinant DNA constructs, unicellular hosts, and
 CC antibodies to TACI protein. Methods are claimed for identifying a ligand
 CC for TACI and for identifying immunosuppressive drugs that selectively
 CC block the action of B lymphocytes without affecting mature T lymphocytes.
 CC TACI can be activated to increase immune system activity, e.g. for
 CC treating infections or cancers. It can be blocked to provide
 CC immunosuppression, e.g. for treating autoimmune and inflammatory

CC conditions such as immune complex- induced vasculitis,
CC glomerulonephritis, haemolytic anaemia, myasthenia gravis, type II
CC collagen-induced arthritis, experimental allergic and hyperacute
CC xenograft rejection, rheumatoid arthritis, systemic lupus erythematosus,
CC transplant rejection, cancer or graft versus host disease
XX

SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
DB 105 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
|||
61 ST 62
165 ST 166

RESULT 10

AAB36312
ID AAB36312 standard; protein; 293 AA.

XX
AC AAB36312;

XX
DT 26-FEB-2001 (first entry)

XX
DE Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.

XX
KW Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;
KW immunosuppressive; neutrotropic; neuroprotective; antiviral; antiallergic;
KW hepatotropic; antidiabetic; antinflammatory; antiulcer; cardiac;
KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;
KW autoimmune disorder.

XX
OS Homo sapiens.

XX
PN WO200058362-A1.

XX
PD 05-OCT-2000.

XX
PF 24-MAR-2000; 2000WO-US007966.

XX
PR 26-MAR-1999; 99US-0126599P.

XX
PR 10-MAR-2000; 2000US-0188208P.

XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PI Ruben SM, Ullrich S, Baker K;

XX
DR WPI; 2000-602359/57.

XX
DR N-PSDB; AAC64602.

XX
PT Nucleic acid encoding a neutrokin-alpha receptor (NAR) such as TR17,
PT useful for producing TR17 protein which is used in the treatment and
PT diagnosis of autoimmune and immunodeficiency disorders.

XX
PS Claim 1; Fig 1; 398pp; English.

XX
CC The present sequence represents the human neutrokin-alpha binding (NAR)
CC protein designated TR17. TR17 has cytostatic, immunosuppressive,
CC neutrotropic, neuroprotective, antiviral, antiallergic, hepatotropic,
CC antidiabetic, antinflammatory, antiulcer, cardiac and ophthalmological
CC activities and can be used in gene therapy. The TR17 protein and
CC antibodies are useful for treating and diagnosing immunodeficiency
CC disorders and autoimmune disorders. The TR17 polypeptides,
CC polynucleotides, antibodies, agonists and/or antagonists are used for
CC treating various other diseases defined in the specification and as
CC research tools for studying the phenotypic effects that result from
CC inhibiting TR17/TR17 ligand interactions on various cell types

SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 3; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
DB 105 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
|||
61 ST 62
165 ST 166

RESULT 11

AAY94000

ID AAY94000 standard; protein; 293 AA.

XX
AC AAY94000;

XX
DT 20-OCT-2000 (first entry)

XX
DE A transmembrane activator and CAML-interactor (TACI).

XX
KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
KW znf4 activity; antibody production; autoimmune disease; amyloidosis;
KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
KW immune response; immunosuppression; graft rejection; joint pain;
KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX
OS Homo sapiens.

XX
PN WO2000040716-A2.

XX
PD 13-JUL-2000.

XX
PF 07-JAN-2000; 2000WO-US000396.

XX
PR 07-JAN-1999; 99US-00226533.

XX
PA (ZYMO) ZYMOGENETICS INC.

XX
PI Gross JA, Xu W, Madden K, Yee DP;

XX
DR WPI; 2000-452538/39.

XX
DR N-PSDB; AAA58558.

XX
PT Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises
PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX
PS Disclosure; Page 149-150; 175pp; English.

XX
CC The present sequence represents a human transmembrane activator and CAML-
CC interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)
CC receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI
CC or BCMA (a related B cell protein) receptor contain a cysteine rich
CC domain, and are used for inhibiting znf4 activity. Znf4 is a TNF
CC ligand. They may also be used for inhibiting BR43x2, TACI or BCMA
CC receptor-ligand engagement associated with activated or resting B
CC lymphocytes, effector T-cells, or with antibody production. The antibody
CC production is associated with an autoimmune disease selected from
CC systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and
CC rheumatoid arthritis. The znf4 activity and BR43x2, TACI or BCMA
CC receptor-ligand engagement is associated with asthma, bronchitis,
CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,

CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
 CC light chain neuropathy, amyloidosis, moderating immune response,
 CC immunosuppression, graft rejection, graft versus host disease,
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
 CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol
 CC or renal emboli

XX SQ Sequence 293 AA;
 Query Match 100.0%; Score 315; DB 3; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1.1e-32;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENKLSPVNLPPELRRQSRGSEVNSDGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
 DB 105 ENKLSPVNLPPELRRQSRGSEVNSDGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
 QY 61 ST 62
 DB 165 ST 166

RESULT 12

AAE09240
 ID AAE09240 standard; protein; 293 AA.

XX AC AAE09240;
 XX DT 19-NOV-2001 (first entry)
 XX DE Human TACI protein.
 XX KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

XX OS Homo sapiens.

XX PN WO200160397-A1.

XX PD 23-AUG-2001.

XX PF 28-NOV-2000; 2000WO-US032378.

XX PR 16-FEB-2000; 2000US-0182938P.

XX PR 22-AUG-2000; 2000US-0226986P.

XX PA (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 PI Yan M;

XX DR WPI; 2001-541628/60.

XX DR N-PSDB; AAD15901.

XX PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists.

XX PS Example 1; Fig 1; 160pp; English.

XX CC The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
 CC TACI or BCMA. The method is useful for treating pathological conditions
 CC or diseases associated with increased TALL-1 and APRIL expression or
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid

CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
 CC present sequence is human TACI protein

XX SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 4; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1.1e-32;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGSEVNSDGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
 DB 105 ENKLSPVNLPPELRRQSRGSEVNSDGRYQGLEHGRSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
 DB 165 ST 166

RESULT 13

AAV71914

ID AAV71914 standard; protein; 293 AA.

XX AC AAV71914;

XX DT 26-MAR-2001 (first entry)

XX DE Human tumour necrosis factor receptor (TACI) protein.

XX KW Human; transmembrane activator and CAML interactor; TACI;
 KW tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;
 KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;
 KW neutrokin alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy;
 KW neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour;
 KW antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis;
 KW rheumatoid arthritis; graft rejection; inflammation; cell proliferation;
 KW cell death; immunoglobulin E-mediated allergic reaction; IgE.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Domain 2..186

XX FT FT /label= Extracellular domain

XX FT FT /note= "Binds with amino acids 123-285 of extracellular
 domain of TACI-L"

XX EN WO200067034-A1.

XX PD 09-NOV-2000.

XX PF 14-APR-2000; 2000WO-US010282.

XX PR 30-APR-1999; 99US-00302863.

XX PA (IMMV) IMMUNEX CORP.

XX PI Goodwin RG, Din WS;

XX DR WPI; 2001-016005/02.

XX DR N-PSDB; AAD02006.

XX PT Use of new interactions between tumor necrosis factor receptors (TACI)

XX PT and TACI ligands to screen candidate molecules for determining agonist

XX PT and antagonist interactions which are used for treating inflammation.

XX PS Claim 10; Fig 1b; 46pp; English.

XX CC The present sequence is a human tumour necrosis factor receptor (TACI)
 CC protein. TACI (transmembrane activator and calcium-signal modulating
 CC cyclophilin ligand (CAML)-interactor) forms a complex with neutrokin
 CC alpha polypeptide (TACI-Ligand). The antagonist or agonist of TACI/TACI-L
 CC complex is useful for modulating an intracellular signalling cascade
 CC mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L complex are
 CC used to inhibit the interaction between TACI and TACI-L for therapeutic

CC purposes to treat tumour and tumour metastasis and to combat various
 CC autoimmune diseases e.g. multiple sclerosis and diabetes, as well as
 CC other disorders, such as viral infection, rheumatoid arthritis, graft
 CC rejection, and immunoglobulin (Ig) E-mediated allergic reactions and
 CC inflammation. The interaction is used to study cellular processes
 CC associated with tumour necrosis factor (TNF)-receptors such as immune
 CC regulation, cell proliferation, cell death and inflammatory responses.
 CC The interaction between the extracellular region of TACI and TACI-L can
 CC be used to further develop understanding of which cell types TACI-L acts
 CC upon

XX Sequence 293 AA;

Query Match 100.0%; Score 315; DB 4; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1.1e-32;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 |||||
 DB 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
 |||||

QY 61 ST 62
 ||
 DB 165 ST 166

·RESULT 14

AAO14130
 ID AAO14130 standard; protein; 293 AA.

XX

AC AAO14130;

XX

DT 02-MAY-2002 (first entry)

XX

DE Human transmembrane activator CAML interactor protein (TACI).

XX

KW Human transmembrane activator CAML interactor protein; TACI; cytostatic;
 KW cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
 KW scleroderma; rheumatoid arthritis; scarring; liver; lung fibrosis;
 KW uterine.

XX Homo sapiens.

OS

XX

PH Key Location/Qualifiers

FT Domain

FT 1..114

FT /label= Extracellular_domain

XX

PN WO200181417-A2.

XX

PD 01-NOV-2001.

XX

XX 27-APR-2001; 2001WO-US040626.

XX

XX 27-APR-2000; 2000US-0199946P.

XX

PA (BIOJ) BIOGEN INC.

PA (APOT-) APOTEC R & D SA.

XX

XX Ambrose C, Thompson J, Schneider P, Rennett P;

XX WPI; 2002-062027/08.

XX N-PSDB; AAK98726.

XX

XX Treating mammal for condition associated with undesired cell

XX proliferation e.g., solid tumor or reducing solid tumor size located in

XX mammal comprises administering transmembrane activator CAML interactor

XX protein reagent.

XX Claim 8; Fig 1; 42pp; English.

XX

CC This sequence represents the human transmembrane activator CAML
 CC interactor protein (TACI). The invention relates to treating a mammal for
 CC a condition associated with undesired cell proliferation (e.g. a solid
 CC tumour, or reducing the size of a solid tumour located on or in a mammal)
 CC comprising administering a transmembrane activator CAML interactor
 CC protein (TACI) reagent. The TACI reagent has cytostatic and vulnerary
 CC activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or
 CC cat) for a condition associated with undesired cell proliferation (e.g.
 CC cancer such as renal cell cancer, Kaposi's sarcoma, breast cancer,
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon
 CC cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma,
 CC pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach
 CC cancer). The method is also useful for treating cellular
 CC hyperproliferation (hyperplasia) such as scleroderma, pannus formation in
 CC rheumatoid arthritis, post-surgical scarring and lung, liver and uterine
 CC fibrosis. The TACI reagent of the invention can extend mean survival time
 CC of a mammal by 25% as compared to the mean survival time of a mammal in
 CC the absence of administering the TACI reagent. The TACI reagent also
 CC reduces the size of the tumour by 25% or more

XX Sequence 293 AA;

Query Match 100.0%; Score 315; DB 5; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1.1e-32;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 |||||

DB 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
 |||||

QY 61 ST 62
 ||

DB 165 ST 166

RESULT 15

ABB81488

ID ABB81488 standard; protein; 293 AA.

XX

AC ABB81488;

XX

DT 02-SEP-2002 (first entry)

XX

DE Human TACI receptor related protein SEQ ID NO:8.

XX

XX

KW Human; Znf12; tumour necrosis factor receptor; cytostatic;

KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;

KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;

KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;

KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;

KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;

KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;

KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;

KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;

KW light chain neuropathy; hypertension; large vessel disease;

KW graft-versus host disease; graft rejection; Crohn's disease.

XX

OS Homo sapiens.

XX

XX WO200238766-A2.

XX

XX 16-MAY-2002.

XX

XX 05-NOV-2001; 2001WO-US047018.

XX

XX 07-NOV-2000; 2000US-0246449P.

XX

XX 20-DEC-2000; 2000US-0257131P.

XX

XX 28-JUN-2001; 2001US-0301715P.

XX

XX 29-AUG-2001; 2001US-0315565P.

XX

XX (ZYMO) ZYMOGENETICS INC.

XX

XX Gross JA, Xu W, Henne RM, Grant FJ;

PI

XX WPI; 2002-508212/54.

XX DR

XX PT Novel isolated human tumor necrosis factor receptor polypeptide, termed

PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage

PT renal failure or renal disease and lymphoma.

XX

XX PS Disclosure; Page 136-137; 154pp; English.

XX

CC The present invention describes a human tumour necrosis factor receptor

CC designated ztnfr12 (I). (I) has cytostatic, immunosuppressive,

CC dermatological, antiinflammatory, neuroprotective, antidiabetic,

CC antirheumatic, antiarthritic, antiaesthatic, nephrotropic and hypotensive

CC activities, and can be used in gene therapy. (I) can be used for

CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12

CC (e.g. ZTNF4), for treating disorders and diseases associated with B

CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for

CC inhibiting the proliferation of tumour cells. (I) is useful for treating

CC autoimmune disorders such as systemic lupus erythematosus, myasthenia

CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,

CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure

CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid

CC leukaemia, nephritis, and pyelonephritis, and for treating renal

CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or

CC ankyloidsis, hypertension, large vessel diseases, graft-versus host

CC disease, graft rejection and Crohn's disease. (I) is useful for

CC modulating the immune system, for regulating B cell responses and

CC development, for modulating development of other cells, antibody

CC production and cytokine production, and for modulating T and B cell

CC communication. The present sequence represents a protein which is given

CC in the exemplification of the present invention

XX SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 5; Length 293;

Best Local Similarity 100.0%; Pred. No. 1.1e-32;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 60

Db |||||

105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62

Db ||

165 ST 166

Search completed: August 12, 2005, 15:11:50

Job time : 75 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2005, 15:07:04 ; Search time 22 Seconds
(without alignments)

210.375 Million cell updates/sec

Title: US-10-068-725-4_COPY_105_166

Perfect score: 315

Sequence: 1 ENKLSPVNLPPELRRQSG.....SPALPGLSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315	100.0	166	2	US-08-810-572A-6
2	315	100.0	166	3	US-09-290-333-6
3	315	100.0	166	4	US-09-782-857A-6
4	315	100.0	166	4	US-09-854-864-15
5	315	100.0	293	2	US-08-810-572A-2
6	315	100.0	293	3	US-09-290-333-2
7	315	100.0	293	4	US-09-782-857A-2
8	315	100.0	293	4	US-09-879-919-22
9	315	100.0	293	4	US-09-848-295-4
10	315	100.0	293	4	US-09-854-864-14
11	310	98.4	397	4	US-09-854-864-18
12	66	21.0	428	4	US-09-252-991A-24431
13	64	20.3	328	4	US-09-252-991A-23205
14	64	20.3	341	4	US-09-252-991A-18308
15	62	19.7	179	4	US-09-252-991A-30669
16	62	19.7	635	4	US-09-252-991A-21514
17	62	19.7	806	1	US-07-980-528-2
18	62	19.7	824	4	US-09-538-092-1242
19	61	19.4	412	4	US-09-252-991A-30252
20	61	19.4	487	4	US-09-248-796A-19251
21	60.5	19.2	336	4	US-09-252-991A-22196
22	60.5	19.2	954	4	US-09-252-991A-32931
23	60	19.0	349	3	US-09-343-011B-1
24	60	19.0	487	4	US-09-252-991A-18581
25	59.5	18.9	203	4	US-09-134-000C-6471
26	59	18.7	242	4	US-09-270-767-43590
27	59	18.7	710	3	US-09-079-812E-2

28	58.5	18.6	214	4	US-09-252-991A-22902	Sequence 22902, A
29	58.5	18.6	261	4	US-09-252-991A-28545	Sequence 28545, A
30	58.5	18.6	453	4	US-09-270-767-44670	Sequence 44670, A
31	58.5	18.6	693	4	US-09-252-991A-24059	Sequence 24059, A
32	58	18.4	172	4	US-09-902-540-12693	Sequence 12693, A
33	58	18.4	511	4	US-09-198-452A-509	Sequence 509, App
34	58	18.4	511	4	US-09-438-185A-475	Sequence 475, App
35	58	18.4	560	4	US-09-949-016-8174	Sequence 8174, App
36	58	18.4	621	3	US-09-026-343-7	Sequence 7, Appli
37	58	18.4	621	3	US-09-362-871-7	Sequence 7, Appli
38	58	18.4	621	4	US-09-949-016-6737	Sequence 6737, Ap
39	58	18.4	1385	2	US-08-687-399-7	Sequence 7, Appli
40	57.5	18.3	190	4	US-09-270-767-46639	Sequence 46639, A
41	57.5	18.3	362	4	US-09-252-991A-30223	Sequence 30223, A
42	57.5	18.3	385	4	US-09-252-991A-25080	Sequence 25080, A
43	57.5	18.3	432	4	US-09-949-016-7465	Sequence 7465, Ap
44	57.5	18.3	584	4	US-09-270-767-43419	Sequence 43419, A
45	57.5	18.3	598	4	US-09-902-540-13703	Sequence 13703, A

ALIGNMENTS

RESULT 1
US-08-810-572A-6

; Sequence 6, Application US/08810572A

; Patent No. 5969102

; GENERAL INFORMATION:

; APPLICANT: Bram, Richard J.

; APPLICANT: von Bulow, Gotz

; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/810,572A

; FILING DATE: 28-FEB-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 1340-1-007

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-487-5800

; TELEFAX: 201-343-1684

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 166 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

US-08-810-572A-6

Query Match 100.0%; Score 315; DB 2; Length 166;

Best Local Similarity 100.0%; Pred. No. 7.7e-34;

```

RESULT 3
US-09-782-857A-6
; Sequence 6, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
;
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857A-6

Query Match 100.0%; Score 315; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 7,7e-34;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSFVNLPPELRQRSGEVENNDNSGRYQGLEHHRGSEASPALPGLKLSADQVALVY 60
DB 105 ENKLRSFVNLPPELRQRSGEVENNDNSGRYQGLEHHRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
DB 165 ST 166

RESULT 4
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

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; TITLE OF INVENTION: BLYS/AGP-3, AND TAC1
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-854-864-15

Query Match      100.0%; Score 315; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.7e-34;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSFVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSFVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62
Db 165 ST 166

RESULT 5
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Floor
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal

Qy 1 ENKLRSFVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSFVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
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US-08-810-572A-2

Query Match      100.0%; Score 315; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSFVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSFVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62
Db 165 ST 166

RESULT 6
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Floor
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-290-333-2

Query Match      100.0%; Score 315; DB 3; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSFVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSFVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
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QY 61 ST 62
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Db 165 ST 166

RESULT 7
US-09-782-857A-2
; Sequence 2, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2

Query Match 100.0%; Score 315; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
|||
Db 105 ENKLSPVNLPPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
||
Db 165 ST 166

RESULT 8
US-09-879-919-22

; Sequence 22, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

Query Match 100.0%; Score 315; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
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Db 105 ENKLSPVNLPPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
||
Db 165 ST 166

RESULT 9
US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; THEREON
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-295-4

Query Match 100.0%; Score 315; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
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Db 105 ENKLSPVNLPPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

Db 105 ENKLRSPVNLPPELRRQSGEVNNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
Db 165 ST 166

RESULT 10
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match 100.0%; Score 315; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ENKLRSPVNLPPELRRQSGEVNNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQSGEVNNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
Db 165 ST 166

RESULT 11
US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18

Query Match 98.4%; Score 310; DB 4; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 105 ENKLRSPVNLPPELRRQSGEVNNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
Qy 61 S 61
Db 165 S 165

RESULT 12
US-09-252-991A-24431
; Sequence 24431, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24431
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24431

Query Match 21.0%; Score 66; DB 4; Length 428;
Best Local Similarity 40.9%; Pred. No. 2.5;
Matches 18; Conservative 8; Mismatches 8; Indels 10; Gaps 2;
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Db 254 LAQQAGHQOH-----HEGLE---EAHPAPDLLLLAADQVA 287

RESULT 13
US-09-252-991A-23205
; Sequence 23205, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23205
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23205

Query Match 20.3%; Score 64; DB 4; Length 328;
Best Local Similarity 31.8%; Pred. No. 3.3;
Matches 21; Conservative 8; Mismatches 23; Indels 14; Gaps 3;
Qy 6 SPVN--LPPELRRQSGEVNNSDNGRYQGL-----EHRGSEASPALPGLKLS 52
Db 165 APVGAALPPAARRQRTGPA--GGHRDGRRTALGVFALRRRLDPDPGPGARPGLDGIEQA 223
Qy 53 ADQVAL 58
Db 224 AHRVAV 229

RESULT 14
US-09-252-991A-18308
; Sequence 18308, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18308
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18308

Query Match 20.3%; Score 64; DB 4; Length 341;
Best Local Similarity 30.5%; Pred. No. 3.4;
Matches 18; Conservative 7; Mismatches 20; Indels 14; Gaps 2;
QY 9 NLPPELRR-----QSGEVENNSDNGRYQGLEHRCGSEASPALPGLKLSADQ 55
Db 144 HLPFPRRRRAARGPERFQRTG--RHGPDRAHRRRPQHRTAVGPRLLPAATVERDQ 200

RESULT 15
US-09-252-991A-30669
; Sequence 30669, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30669
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30669

Query Match 19.7%; Score 62; DB 4; Length 179;
Best Local Similarity 41.3%; Pred. No. 2.7;
Matches 19; Conservative 4; Mismatches 19; Indels 4; Gaps 2;
QY 10 LPPELRRQSGEVENNSDNGRY--QGLEHRCGSEASPALPGLKLSA 53
Db 91 LHPQLRQRPANHFGTTTERRRCDQGLRRPGSGAD--LFGLRSA 134

Search completed: August 12, 2005, 15:15:35
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2005, 15:11:59 ; Search time 157 Seconds
(without alignments)
154.342 Million cell updates/sec

Title: US-10-068-725-4_COPY_105_166

Perfect score: 315
Sequence: 1 ENKLSPVNLPELRQRSG.....SPALPGLKLSADQVALVYST 62

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Total number of hits satisfying chosen parameters: 1755696

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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17: /cgn2_6/ptodata/2/pubaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubaa/US10F_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	315	100.0	166	9	US-09-855-158-15
3	315	100.0	166	14	US-10-293-816-6
4	315	100.0	246	17	US-10-626-914-14
5	315	100.0	246	17	US-10-861-049-53
6	315	100.0	246	20	US-11-021-874-53
7	315	100.0	247	17	US-10-485-489-14
8	315	100.0	265	17	US-10-626-914-17
9	315	100.0	265	17	US-10-485-489-19
10	315	100.0	265	17	US-10-861-049-36
11	315	100.0	265	20	US-11-021-874-36

Sequence 22, Appl	9	US-09-879-919-22	293	100.0	315	100.0
Sequence 14, Appl	9	US-09-854-864-14	293	100.0	315	100.0
Sequence 14, Appl	9	US-09-855-158-14	293	100.0	315	100.0
Sequence 2, Appl	9	US-09-961-376-2	293	100.0	315	100.0
Sequence 42, Appl	9	US-09-779-050A-42	293	100.0	315	100.0
Sequence 2, Appl	10	US-09-302-863-2	293	100.0	315	100.0
Sequence 2, Appl	10	US-09-855-564-2	293	100.0	315	100.0
Sequence 1650, Ap	13	US-10-087-192-1650	293	100.0	315	100.0
Sequence 4, Appl	13	US-10-084-971-2	293	100.0	315	100.0
Sequence 46, Appl	14	US-10-068-725-4	293	100.0	315	100.0
Sequence 2, Appl	14	US-10-151-882-46	293	100.0	315	100.0
Sequence 8, Appl	14	US-10-293-816-2	293	100.0	315	100.0
Sequence 2, Appl	14	US-10-008-063-8	293	100.0	315	100.0
Sequence 22, Appl	14	US-10-152-363A-2	293	100.0	315	100.0
Sequence 1, Appl	14	US-10-268-951-22	293	100.0	315	100.0
Sequence 4, Appl	15	US-10-258-368-1	293	100.0	315	100.0
Sequence 7, Appl	15	US-10-618-797-4	293	100.0	315	100.0
Sequence 27, Appl	16	US-10-742-634-7	293	100.0	315	100.0
Sequence 4, Appl	16	US-10-748-112-27	293	100.0	315	100.0
Sequence 3, Appl	17	US-10-684-149-4	293	100.0	315	100.0
Sequence 3, Appl	17	US-10-626-914-3	293	100.0	315	100.0
Sequence 25, Appl	17	US-10-485-489-3	293	100.0	315	100.0
Sequence 25, Appl	17	US-10-861-049-25	293	100.0	315	100.0
Sequence 12, Appl	20	US-11-021-874-25	293	100.0	315	100.0
Sequence 18, Appl	301	US-10-258-368-12	301	100.0	315	100.0
Sequence 18, Appl	37	US-09-854-864-18	37	98.4	310	98.4
Sequence 43, Appl	397	US-09-855-158-18	397	95.4	310	95.4
Sequence 15, Appl	9	US-09-779-050A-43	291	91.1	287	91.1
Sequence 47, Appl	15	US-10-258-368-15	404	88.7	41	279.5
Sequence 50, Appl	9	US-09-779-050A-47	57	82.5	42	260
Sequence 1647, Ap	14	US-10-152-363A-50	392	44.9	43	141.5
Sequence 56, Appl	13	US-10-087-192-1647	249	27.0	44	85
Sequence 181850,	14	US-10-152-363A-56	357	21.6	45	68
	15	US-10-424-599-181850	305			

ALIGNMENTS

RESULT 1
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match	100.0%	Score 315;	DB 9;	Length 166;
Best Local Similarity	100.0%	Pred. No. 1.7e-30;		
Matches	62;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
Qy	1	ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY	60	
Db	105	ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY	164	
Qy	61	ST 62		

Db 165 ST 166

RESULT 2

US-09-855-158-15

; Sequence 15, Application US/09855158

; Publication No. US20020086018A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL

; FILE REFERENCE: A-686A

; CURRENT APPLICATION NUMBER: US/09/855,158

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 15

; LENGTH: 166

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-855-158-15

Query Match 100.0%; Score 315; DB 9; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.7e-30;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGEASPALPGLKLSADQVALVY 60

Db 105 ENKLSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGEASPALPGLKLSADQVALVY 164

QY 61 ST 62

Db 165 ST 166

RESULT 3

US-10-293-816-6

; Sequence 6, Application US/10293816

; Publication No. US20030082173A1

; GENERAL INFORMATION:

; APPLICANT: Bram, Richard J.

; APPLICANT: Von Bulow, Gotz

; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

; FILE REFERENCE: 44158/254623

; CURRENT APPLICATION NUMBER: US/10/293,816

; CURRENT FILING DATE: 2002-11-12

; PRIOR APPLICATION NUMBER: US 09/782,857

; PRIOR FILING DATE: 2001-02-14

; PRIOR APPLICATION NUMBER: US 09/290,333

; PRIOR FILING DATE: 1999-04-12

; PRIOR APPLICATION NUMBER: US 08/810,572

; PRIOR FILING DATE: 1997-03-03

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 166

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-293-816-6

Query Match 100.0%; Score 315; DB 14; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.7e-30;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGEASPALPGLKLSADQVALVY 60

Db 105 ENKLSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGEASPALPGLKLSADQVALVY 164

QY 61 ST 62

Db 165 ST 166

RESULT 4

US-10-626-914-14

; Sequence 14, Application US/10626914

; Publication No. US20050043516A1

; GENERAL INFORMATION:

; APPLICANT: CHUNTHARAPAI, ANAN

; APPLICANT: GREWAL, IOBAL

; APPLICANT: KIM, KYUNG JIN

; APPLICANT: YAN, MINHONG

; TITLE OF INVENTION: TAC1 Antibodies and Uses Thereof

; FILE REFERENCE: P1942R1

; CURRENT APPLICATION NUMBER: US/10/626,914

; CURRENT FILING DATE: 2003-07-25

; PRIOR APPLICATION NUMBER: US 60/398,530

; PRIOR FILING DATE: 2002-07-25

; NUMBER OF SEQ ID NOS: 17

; SEQ ID NO 14

; LENGTH: 246

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-626-914-14

Query Match 100.0%; Score 315; DB 17; Length 246;

Best Local Similarity 100.0%; Pred. No. 2.8e-30;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGEASPALPGLKLSADQVALVY 60

Db 59 ENKLSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGEASPALPGLKLSADQVALVY 118

QY 61 ST 62

Db 119 ST 120

RESULT 5

US-10-861-049-53

; Sequence 53, Application US/10861049

; Publication No. US20050095243A1

; GENERAL INFORMATION:

; APPLICANT: Andrew Chan

; APPLICANT: Qian Gong

; APPLICANT: Flavius Martin

; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS

; FILE REFERENCE: P2040R1US

; CURRENT APPLICATION NUMBER: US/10/861,049

; CURRENT FILING DATE: 2004-06-04

; PRIOR APPLICATION NUMBER: US 60/476,531

; PRIOR FILING DATE: 2003-06-06

; PRIOR APPLICATION NUMBER: US 60/476,481

; PRIOR FILING DATE: 2003-06-05

; PRIOR APPLICATION NUMBER: US 60/476,414

; PRIOR FILING DATE: 2003-06-05

; NUMBER OF SEQ ID NOS: 145

; SEQ ID NO 53

; LENGTH: 246

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-861-049-53

Query Match 100.0%; Score 315; DB 17; Length 246;

Best Local Similarity 100.0%; Pred. No. 2.8e-30;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGEASPALPGLKLSADQVALVY 60

Db 59 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 118
Qy 61 ST 62
Db 119 ST 120

RESULT 6
US-11-021-874-53
; Sequence 53, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021,874
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/861,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 53
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-874-53

Query Match 100.0%; Score 315; DB 20; Length 246;
Best Local Similarity 100.0%; Pred. No. 2.8e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 59 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 118

Qy 61 ST 62
Db 119 ST 120

RESULT 7
US-10-485-489-14
; Sequence 14, Application US/10485489
; Publication No. US20050070689A1
; GENERAL INFORMATION:
; APPLICANT: Dixit, Vishva
; APPLICANT: Grewal, Iqbal
; APPLICANT: Ridgway, John
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: TACIS and BR3 Polypeptides and Uses Thereof
; FILE REFERENCE: 11669.175USWO
; CURRENT APPLICATION NUMBER: US/10/485,489
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/US02/23487
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/310,114
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/377,171
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 14
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-489-14

Query Match 100.0%; Score 315; DB 17; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.8e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 59 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 118

Qy 61 ST 62
Db 119 ST 120

RESULT 8
US-10-626-914-17
; Sequence 17, Application US/10626914
; Publication No. US20050043516A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: CHUNTHARAPAI, ANAN
; APPLICANT: GREWAL, IQBAL
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: YAN, MINHONG
; TITLE OF INVENTION: TACI Antibodies and Uses Thereof
; FILE REFERENCE: P1942R1
; CURRENT APPLICATION NUMBER: US/10/626,914
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,530
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 17
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-626-914-17

Query Match 100.0%; Score 315; DB 17; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62
Db 165 ST 166

RESULT 9
US-10-485-489-19
; Sequence 19, Application US/10485489
; Publication No. US20050070689A1
; GENERAL INFORMATION:
; APPLICANT: Dixit, Vishva
; APPLICANT: Grewal, Iqbal
; APPLICANT: Ridgway, John
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: TACIS and BR3 Polypeptides and Uses Thereof
; FILE REFERENCE: 11669.175USWO
; CURRENT APPLICATION NUMBER: US/10/485,489
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/US02/23487
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/310,114
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/377,171
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 19
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-489-19

US-10-485-489-19

Query Match 100.0%; Score 315; DB 17; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
|||||
Db 105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
|||||

QY 61 ST 62
||
Db 165 ST 166

RESULT 10

US-10-861-049-36
; Sequence 36, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 36
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-049-36

Query Match 100.0%; Score 315; DB 17; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
|||||
Db 105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
|||||

QY 61 ST 62
||
Db 165 ST 166

RESULT 11

US-11-021-874-36
; Sequence 36, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021,874
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/861,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05

; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 36
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-874-36

Query Match 100.0%; Score 315; DB 20; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
|||||
Db 105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
|||||

QY 61 ST 62
||
Db 165 ST 166

RESULT 12

US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

Query Match 100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.5e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
|||||
Db 105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
|||||

QY 61 ST 62
||
Db 165 ST 166

RESULT 13

US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: ELIS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match 100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.5e-30; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 0

Qy 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
||
Db 165 ST 166

RESULT 14

US-09-855-158-14
; Sequence 14, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-14

Query Match 100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.5e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
||
Db 165 ST 166

RESULT 15

US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
; FILE REFERENCE: PF524P1
; CURRENT APPLICATION NUMBER: US/09/961,376
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-376-2

Query Match 100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.5e-30; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 0

Qy 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
||
Db 165 ST 166

Search completed: August 12, 2005, 15:26:34
Job time : 158 secs

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Db 870 EEEQPTAKIPTDTHREHSHPDPPDPDDELNNNSNNNS----SLQHDGSSSP 918

RESULT 3

S22765
heterogeneous ribonuclear particle protein U - human
N;Alternate names: hnRNP protein U; phosphoprotein pp120; scaffold attachment factor A
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S22765; S42726; B55996
R;Kiledjian, M.; Dreyfuss, G.
EMBO J. 11, 2655-2664, 1992
A;Title: Primary structure and binding activity of the hnRNP U protein: binding RNA through
A;Reference number: S22765; MUID: 92331618; PMID:1628625
A;Accession: S22765
A;Molecule type: mRNA
A;Residues: 1-806 <KIL>
A;Cross-references: UNIPROT:Q00839; EMBL:X65488; NID:G32357; PIDN:CAA46472.1; PID:G32358
R;Fackelmayr, F.O.; Richter, A.
Biochim. Biophys. Acta 1217, 232-234, 1994
A;Title: hnRNP-U/SAP-A is encoded by two differentially polyadenylated mRNAs in human cells
A;Reference number: S42726; MUID: 94154006; PMID:7509195
A;Accession: S42726
A;Molecule type: mRNA
A;Residues: 802-806 <FAC>
R;Jordan, P.; Heid, H.; Kinzel, V.; Kuebler, D.
Biochemistry 33, 14696-14706, 1994
A;Title: Major cell surface-located protein substrates of an ecto-protein kinase are homophilic
A;Reference number: A55996; MUID: 95086063; PMID:7993898
A;Accession: B55996
A;Molecule type: protein
A;Residues: 'XXX', 5-7; 237-246; 444-454, 'XX', 457 <JOR>
A;Experimental source: surface-labelled HeLa cells
C;Genetics:
A;Gene: GDB:HNRPNU
A;Cross-references: GDB:347585
C;Keywords: ATP; nucleotide binding; nucleus; P-loop; phosphoprotein
F;495-492/Region: nucleotide-binding motif A (P-loop)
F;491/Binding site: ATP (Lys) #status predicted

Query Match 19.7%; Score 62; DB 2; Length 806;
Best Local Similarity 31.6%; Pred. No. 27;
Matches 18; Conservative 7; Mismatches 20; Indels 12; Gaps 2;

Qy 3 KLRSPVNLPELRQRQGEVNNSDNSGRQY-----GLEHRCSEASPALPG 48
| | | | | : : : : : | | | | |
Db 651 KEESKALPPE-KKQNTGSKSKNKYKGNQFNRRGGGHRGGLNMRGNFRGGAPG 706

RESULT 4

T23644
hypothetical protein M01E5.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23644
R;Dobson, R.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19777
A;Accession: T23644
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-250 <WIL>
A;Cross-references: UNIPROT:O45690; EMBL:Z93385; PIDN:CAB07636.1; GSPDB:IGN00019; CESP:M01E5.4
A;Experimental source: clone M01E5
C;Genetics:
A;Gene: CESP:M01E5.4
A;Map position: 1
A;Introns: 83/1; 182/3

Query Match 19.5%; Score 61.5; DB 2; Length 250;
Best Local Similarity 36.7%; Pred. No. 8.3;
Matches 18; Conservative 4; Mismatches 26; Indels 1; Gaps 1;

C:Genetics:
A:Gene: At2g19950
A:Map position: 2

Query Match 19.2%; Score 60.5; DB 2; Length 713;
Best Local Similarity 35.5%; Pred. No. 36;
Matches 22; Conservative 9; Mismatches 24; Indels 7; Gaps 2;

QY 1 ENKLRSPVNLPPPELRRQSRGEVNNDS-----GRYQGLEHRRGSEASPALPGLKLSA 53
Db 385 EGKLSLQALRELTATERRAEBERSAHNATKMAAMERERELEHRAVDASTALVRIQRIA 444
QY 54 DQ 55
Db 445 DE 446

RESULT 10
T22938
hypothetical protein F58G11.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22938
R:Percy, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19640
A:Accession: T22938
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-717 <WIL>
A:Cross-references: UNIPROT:Q9XVM1; EMBL:Z81094; PIDN:CA803149.1; GSPDB:GN00023; CESP:F
A:Experimental source: clone F58G11
C:Genetics:
A:Gene: CESP:F58G11.5
A:Map position: 5
A:Introns: 41/1; 76/1; 122/3; 169/3; 220/2; 338/1; 429/3; 471/2; 632/2; 669/3

Query Match 19.0%; Score 60; DB 2; Length 717;
Best Local Similarity 43.6%; Pred. No. 42;
Matches 17; Conservative 1; Mismatches 15; Indels 6; Gaps 1;

QY 5 RSPVNLPPPELRRQSRGEVNNDSGRYQGLEHRRGSEAS 43
Db 574 RSPSRGSPRRQRS-----SSNSRSGSSSSSSSS 606

RESULT 11
T40615
transcription initiation factor iif, beta subunit - fission yeast (Schizosaccharomyces
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40615
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z21941
A:Accession: T40615
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-307 <LYN>
A:Cross-references: UNIPROT:O94424; EMBL:AL034563; PIDN:CAA22523.1; GSPDB:GN00067; SPDB:
A:Experimental source: strain 972h-; cosmid c660
C:Genetics:
A:Gene: SPDB:SPBC660.03c
A:Map position: 2
A:Introns: 175/3; 223/3
C:Keywords: transcription initiation

Query Match 18.7%; Score 59; DB 2; Length 307;
Best Local Similarity 30.2%; Pred. No. 21;
Matches 13; Conservative 8; Mismatches 14; Indels 8; Gaps 1;

QY 13 ELRRQSRGEVNNDSGRYQGLEHRRGSEASPALPGLKLSADQ 55
Db 13 ELRRQSRGEVNNDSGRYQGLEHRRGSEASPALPGLKLSADQ 55

262 ELRNOASQSESS-----IDHTGKNTSPDNPGTNAEEDE 296

RESULT 12

A46216
transcription factor Skn-1, splice form a - rat
N;Alternate names: Skn-1a
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 05-Dec-1997
R;Accession: A46216
C;Accession: B.; Schonemann, M.D.; Flynn, S.E.; Pearse II, R.V.; Singh, H.; Rosenfeld, M.
Science 260, 78-82, 1993
A;Title: Skn-1a and Skn-1i: two functionally distinct Oct-2-related factors expressed in
A;Reference number: A46216; MUID:93219836; PMID:7682011
A;Accession: A46216
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-430 <AND>
A;Cross-references: GB:I23862; NID:g393220
A;Note: sequence extracted from NCBI backbone (NCBI:P128572)
C;Superfamily: transcription factor Oct-2; homeobox homology; POU domain homology
C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulation
F;183-250/Domain: POU domain homology <POU>
F;275-331/Domain: homeobox homology <HOX>

Query Match 18.7%; Score 59; DB 1; Length 430;
Best Local Similarity 24.1%; Pred. No. 31;
Matches 20; Conservative 11; Mismatches 20; Indels 32; Gaps 3;

QV 8 VNLPEL-----RRQSGEVENNSDNG-----RYQGLEHR 38

Db 2 VNLEPMLSEIKMSGVDADSTARSTPGQVESGNDRGLDFNRQIKTEDLGDTHESLSHR 61

QY 39 G---SEASPALPGLKLSADQVAL 58

62 PCHLTEGPTMMPGNOMSGDMASL 84

RESULT 13

catalase (RC 1.11.1.6) precursor - fission yeast (Schizosaccharomyces pombe)
 C|Species: Schizosaccharomyces pombe
 C|Date: 27-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
 C|Accession: JC4164; PC4041; T41598
 R|Nakagawa, C.W.; Mutoh, N.; Hayaashi, Y.
 J. Biochem. 118, 109-116, 1995
 A|Title: Transcriptional regulation of catalase gene in the fission yeast Schizosaccharomyces pombe
 A|Reference number: JC4164; MUID:96015157; PMID:8537298
 A|Accession: JC4164
 A|Molecule type: DNA
 A|Residues: 1-512 <NAK>
 A|Cross-references: UNIPROT:P55306; GB:D55675; NID:g1905773; PIDN:BAA09526.1; PID:g871977
 A|Accession: PC4041
 A|Molecule type: protein
 A|Residues: 277-286; 421-431 <NA2>
 R|Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
 submitted to the EMBL Data Library, October 1998
 A|Reference number: Z22003
 A|Accession: T41598
 A|Status: preliminary; translated from GB/EMBL/DDBB
 A|Molecule type: DNA
 A|Residues: 1-512 <LYN>
 A|Cross-references: EMBL:AL031825; PIDN:CAA21232.1; GSPDB:GN00068; SPDB:SPCC757.07c
 A|Experimental source: strain 972h-; cosmid c757
 C|Comment: This enzyme is induced 8-fold in response to low concentrations of hydrogen peroxide
 C|Genetics:
 A|Gene: ctal; SPDB:SPCC757.07c
 A|Map position: 3
 C|Superfamily: catalase
 C|Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
 F|1-27/Domain: signal sequence #status predicted <SIG>
 F|28-512/Product: catalase #status predicted <NAT>
 F|60_99_133/Active site: His, Ser, Asn #status predicted

F:344/Binding site: heme iron (Tyr) (axial ligand) #status predicted

Query Match 18.7%; Score 59; DB 2; Length 512;

Best Local Similarity	32.6%;	Pred. No. 37;	
Matches	14;	Conservative	8;
Mismatches	21;	Indels	0;
Caps	0;		

QY 17 QRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALV 59

297 ORVGRFTLNONPTNFFADIEOAGFSPSHMVPGIEVSADPVLQV 339

RESULT 14

T42369
 catalase [EC 1.11.1.6] - fission yeast (*Schizosaccharomyces pombe*) (fragment)
 C:Species: *Schizosaccharomyces pombe*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 C:Accession: T42369
 R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
 DNA Res. 4, 363-369, 1997
 A:Title: Identification of open reading frames in *Schizosaccharomyces pombe*
 A:Reference number: Z17323; MUID:98162722; PMID:9501991
 A:Accession: T42369
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-532 <YOS>
 A:Cross-references: EMBL:D89126; NID:g1749459; PIDN:BAAL3788.1; PID:g1749460
 A:Experimental source: strain PR745

C;Function:

A;Description: catalyzes the conversion of two of mole

C;Superfamily: catalase

C;Keywords: heme; iron; metalloprotein; oxidoreductase
E-00 110 152/Active site. Uic. Soc. Non #status predicted

F;80,119,153/Active site:	H18, Ser,	ASN #status predicted
F:364/Binding site:	heme iron (Tyr)	(axial ligand) #status predicted

Query Match 18.7%; Score 59; DB 2; Length 532;

BEST LOCAL SIMILARITY 32.6%; FREQ. NO: 33;
Matches 14: Conservative 8: Mismatches 21: Indels 0: Gaps 0:

DATE 10/10/2000

Qy 17 QRSGEVNNSDNSGRYQGLEHRCGSEASPGLKLSADQVALV 59

RESULT 15

T10696
legumin-like protein 1 - common buckwheat
C:Species: Fagopyrum esculentum (common buckwheat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10696
R:Fujino, K.; Funatsuki, H.; Inada, M.; Shimono, Y.; Kikuta, Y.
submitted to the EMBL Data Library, September 1996
A:Description: Expression and sequence analysis of cDNAs corresponding to genes
A:Reference number: Z17081
A:Accession: T10696
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-565 <FUJ>
A:Cross-references: UNIPROT:O23878; EMBL:D87980
A:Experimental source: cv. Kitayuki; immature seed; 14 days after anthesis
C:Superfamily: glycinin
C:Keywords: seed; storage protein

Query Match	18.7%	Score 59;	DB 2;	Length 565;
Best Local Similarity	28.2%	Pred. NO.	42;	

BEST LOCAL SIMILARITY 28.23; FREQ. NO: 42;
Matches 24; Conservative 6; Mismatches 23; Indels 32; Gaps 3;

[illegible]

QY 3 KLRSPVNLPPELRRQSRGVEVNNSDNSGRYQGLE-----HRGSEAS----- 43

Db 350 KLRVPEYEEELQREG---DKRGGGGRSNGLEQAFCNLKFKQNVNRPSPRADVFENPRAG 406

Qy 44 -----PALPGLKLSADQVAL 58

4000 3000 2000 1500 1000 500

Search completed: August 12, 2005, 15:12:18
Job time : 24 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2005, 15:05:54 ; Search time 167 Seconds
(without alignments)

190.113 Million cell updates/sec

Title: US-10-068-725-4_COPY_105_166

Perfect score: 315

Sequence: 1 ENKLSPVNLPPELRRQSG.....SPALPGLKLSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315	100.0	247	2 Q7Z6F5	Q7Z6F5 homo sapien
2	315	100.0	293	1 T13X HUMAN	O14836 homo sapien
3	141.5	44.9	249	1 T13X_MOUSE	Q9et35 mus musculus
4	140	44.4	156	2 Q9N146	Q9N146 macaca mula
5	84.5	26.8	702	2 Q9VH96	Q9VH96 drosophila
6	66	21.0	480	2 Q7YT18	Q7YT18 strongyloce
7	66	21.0	480	2 Q9GUY6	Q9GUY6 hemientrot
8	66	21.0	497	2 Q942X2	Q942X2 oryza sativ
9	66	21.0	509	2 Q98KE4	Q98KE4 thizobium l
10	66	21.0	546	2 Q7VBZ9	Q7VBZ9 prochloroco
11	66	21.0	554	2 Q9JHT9	Q9JHT9 mus musculus
12	66	21.0	620	2 Q923H2	Q923H2 mus musculus
13	66	21.0	710	2 Q8CHT1	Q8CHT1 mus musculus
14	65.5	20.8	677	2 Q8TEJ7	Q8TEJ7 homo sapien
15	65	20.6	835	2 Q8KRE4	Q8KRE4 agrobacteri
16	64.5	20.5	87	2 Q9AY96	Q9AY96 ictalurus p
17	64.5	20.5	358	2 Q96BE7	Q96BE7 homo sapien
18	64	20.3	433	2 Q7XK69	Q7XK69 oryza sativ
19	63.5	20.2	800	2 Q6BJB7	Q6BJB7 debaryomyce
20	63.5	20.2	1665	2 Q8F1Z5	Q8F1Z5 candida gla
21	63	20.0	3374	2 Q8J3J3	Q8J3J3 montana myo
22	62.5	19.8	315	2 Q7J3U6	Q7J3U6 mycobacteri
23	62.5	19.8	1092	2 Q7KVZ8	Q7KVZ8 drosophila
24	62.5	19.8	1108	2 Q8MR12	Q8MR12 drosophila
25	62.5	19.8	1741	2 Q46095	Q46095 drosophila
26	62.5	19.8	1741	2 Q9W517	Q9W517 drosophila
27	62.5	19.8	1768	2 Q24153	Q24153 drosophila
28	62.5	19.8	6858	2 Q7QUW1	Q7QUW1 giardia lam
29	62	19.7	824	1 ROU HUMAN	Q00839 homo sapien
30	61.5	19.5	250	2 Q45690	Q45690 caenorhabdi
31	61.5	19.5	322	2 Q8PY32	Q8PY32 methanosarc

RESULT 1

Q7Z6F5 ID Q7Z6F5 PRELIMINARY; PRT; 247 AA.
AC Q7Z6F5; 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 26, Last annotation update)
DE Transmembrane activator and CAML interactor.
DE Transmembrane activator and CAML interactor.
GN Name=TNFRSF13B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY302137; AAP57629.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Transmembrane.
SQ SEQUENCE 247 AA; 26664 MW; 850E1F4C2578E8E6 CRC64;

Query Match 100.0%; Score 315; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 7.5e-29;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLSPVNLPPELRRQSGEVNNSDNGRYOGLEHRSSEASPALPGLKLSADQVALVY 60
|||
Db 59 ENKLSPVNLPPELRRQSGEVNNSDNGRYOGLEHRSSEASPALPGLKLSADQVALVY 118
|||

Qy 61 ST 62

Db 119 ST 120

RESULT 2

T13X HUMAN ID T13X HUMAN STANDARD; PRT; 293 AA.
AC O14836; 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 44, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
DE Name=TNFRSF13B; Synonyms=TACI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA von Buelow G.-U., Bram R.J.;

DOI=10.1126/science.278.5335.138;

RT "NF-AT activation induced by a CAML-interacting member of the tumor
RT necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedini T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D.,
RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT high affinity receptor for TNF family members APRIL and BLyS.";
RL J. Biol. Chem. 275:35478-35485(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=2170284; PubMed=10973284; DOI=10.1038/79802;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc H., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
RN [5]
RP INTERACTIONS WITH TRAF2 AND TRAF5.
RX MEDLINE=20341628; PubMed=10880535;
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
RA Meng S.Y., Boyle W.J., Hsu H.;
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT factor family member involved in B cell regulation.";
RL J. Exp. Med. 192:137-143(2000).
RN [6]
RP FUNCTION. Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLyS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity.
CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAMLG with its C-terminus.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC intestine and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
CC
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CC -----
DR EMBL; AF023614; AAC51790.1; -;
DR EMBL; BC028072; AAH28072.1; -;
DR HSSP; O9Y275; 1OOD.
DR Genew; HGNC:18153; TNFRSF13B.
DR MIM; 604907; -;
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0004872; F: receptor activity; TAS.
DR GO; GO:0007166; P: cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001368; TNFR_C6.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; FALSE_NEG.
KW Glycoprotein; Immune response; Receptor; Repeat; Signal-anchor;
KW Transmembrane.
FT DOMAIN 1 165 Extracellular (Potential).
FT TRANSMEM 166 186 Signal-anchor for type III membrane
FT FT 187 293 protein (Potential).
FT REPEAT 33 67 Cytoplasmic (Potential).
FT DISULFID 34 47 TNFR-Cys 1.
FT DISULFID 50 62 By similarity.
FT DISULFID 54 66 By similarity.
FT DISULFID 71 86 By similarity.
FT DISULFID 89 100 By similarity.
FT DISULFID 93 104 By similarity.
FT CARBOHYD 128 128 N-linked (GlcNAc. . .) (Potential).
FT CONFLICT 251 251 P -> L (in Ref. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

Query Match 100.0%; Score 315; DB 1; Length 293;
Best Local Similarity 100.0%; Pred. No. 9.3e-29;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQRSGEVENNSDGRYQGLEHKGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLSPVNLPPELRRQRSGEVENNSDGRYQGLEHKGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
Db 165 ST 166

RESULT 3
TI3X MOUSE
ID TI3X MOUSE STANDARD; PRT; 249 AA.
AC Q9ET35; Q9DBZ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
DE Name=TNFRsf13b; Synonyms=Taci;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen.
RX MEDLINE=21177554; PubMed=10881172; DOI=10.1038/76889;
RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
RT "Identification of a receptor for BLyS demonstrates a crucial role in
RT humoral immunity.";
RL Nat. Immunol. 1:37-41(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
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 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
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 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Havaehizaki Y.,
 "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 Nature 420:563-573(2002).
 [3]
 FUNCTION.
 MEDLINE=20341628; PubMed=10880535;
 Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 Theill L.E., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R.,
 Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Bellant J.,
 Meng S.-Y., Boyle W.J., Heu H.;
 "TACI is a TRAP-interacting receptor for TALL-1, a tumor necrosis
 factor family member involved in B cell regulation.";
 J. Exp. Med. 192:137-143(2000).
 [4]
 FUNCTION.
 MEDLINE=21322748; PubMed=11429548; DOI=10.1038/89782;
 Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
 Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 "TACI-ligand interactions are required for T cell activation and
 collagen-induced arthritis in mice";
 Nat. Immunol. 2:632-637(2001).
 -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS
 that binds both ligands with similar high affinity. Mediates
 calcineurin-dependent activation of NF-AT, as well as activation
 of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 cell function and the regulation of humoral immunity (By
 similarity).
 -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 domain of CAMLG with its C-terminus (By similarity).
 -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 -1- SIMILARITY: Contains 2 TNFR-Cys repeats.

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 EMBL; AF257673; AAC00081.1; -;
 EMBL; AK004668; BAB23457.1; -;
 MGD; MGI:1889411; Tnftr3f3b.
 DR GO; GO:0005887; C: integral to plasma membrane; IDA.
 DR GO; GO:0005031; F: tumor necrosis factor receptor activity; IDA.
 DR InterPro; IPR001368; TNFR_c6.
 DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.

DR PROSITE; PS00050; TNFR_NGFR_2; FALSE_NEG.
 KW Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.
 FT DOMAIN 1 128 Extracellular (Potential).
 FT TRANSMEM 129 149 Signal-anchor for type III membrane
 FT PROTEIN (Potential).
 FT CYTOPLASMIC (Potential).
 FT DOMAIN 150 249 Cytoplasmic (Potential).
 FT REPEAT 5 38 TNFR-Cys 1.
 FT REPEAT 42 76 TNFR-Cys 2.
 FT DISULFID 6 19 By similarity.
 FT DISULFID 22 34 By similarity.
 FT DISULFID 26 38 By similarity.
 FT DISULFID 43 58 By similarity.
 FT DISULFID 61 72 By similarity.
 FT DISULFID 65 76 By similarity.
 FT CONFLICT 137 137 I -> F (in Ref. 2).
 SQ SEQUENCE 249 AA; CB2F2D61C2931D81 CRC64;
 Query Match 44.9%; Score 141.5; DB 1; Length 249;
 Best Local Similarity 53.2%; Pred. No. 2.2e-08;
 Matches 33; Conservative 7; Mismatches 13; Indels 9; Gaps 2;
 QY 1 ENKLRSPVNLPPELRRQRSGEVNNDNSGRVYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 DB 77 EKPRSQANLQPELGRPQAGEVEVRSDNSGRHQSGE-----PGLRLSSDQLTL-Y 127
 QY 61 ST 62
 DB 128 CT 129
 RESULT 4
 Q9N146 PRELIMINARY; PRT; 156 AA.
 ID Q9N146
 AC Q9N146
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Transmembrane activator (Fragment).
 GN Name=NF-AT;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Arredondo J.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF227558; AAF73400.1; -;
 DR GO; GO:0016021; C: integral to membrane; IEA.
 KW Transmembrane.
 FT NON TER 1
 SQ SEQUENCE 156 AA; 16170 MW; 8AD74E4D17D511D0 CRC64;
 Query Match 44.4%; Score 140; DB 2; Length 156;
 Best Local Similarity 96.6%; Pred. No. 1.8e-08;
 Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 34 GLEHGRGSEASPALPGLKLSADQVALVYST 62
 DB 1 GLEHGRGSEASPALPGLKLSADQVALVYST 29
 RESULT 5
 Q9VH96 PRELIMINARY; PRT; 702 AA.
 ID Q9VH96
 AC Q9VH96
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE CG8358-PA (GH26575p).
 GN ORFNames=CG8358;
 OS Drosophila melanogaster (Fruit fly).

[illegible]

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QY      54 DOVA 57
Db      461 PR7A 464

RESULT 9
Q98KE4  Q98KE4      PRELIMINARY;      PRT;      509 AA.
AC      Q98KE4;
DT      01-OCT-2001 (TrEMBLrel. 18, Created)
DT      01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      T-imethylamine methyltransferase; MttB.
GN      OrderedLocusNames=ml1516;
OS      Rhizobium loti (Mesorhizobium loti).
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC      Phyllobacteriaceae; Mesorhizobium.
OX      NCBI_TaxID=381;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MAFF303099;
RX      MEDLINE=21082930; PubMed=11214968;
RA      Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA      Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA      Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA      Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA      Takeuchi C., Yamada M., Tabata S.;
RT      "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT      Mesorhizobium loti.";
RL      DNA Res. 7:331-338(2000).
DR      GO: GO:0008168; F:methyltransferase activity; IEA.
DR      GO: GO:0016740; F:transferase activity; IEA.
DR      InterPro: IPR010426; MTTB.
DR      Pfam: PF06253; MTTB; 1.
KW      Complete proteome; Methyltransferase; Transferase.
SQ      SEQUENCE 509 AA; 54430 MW; 283A0E396332A2AC CRC64;

Query Match      21.0%; Score 66; DB 2; Length 509;
Best Local Similarity 36.0%; Pred. No. 41;
Matches 18; Conservative 7; Mismatches 19; Indels 6; Gaps 1;

QY      13 ELRRQSRGSEVNNDSGRYQGLEHGRGSEASPALGKLSDQV 62
Db      4 ERRRGITGEAGSSRRPNVRSUK-----NPFLPQIFSDQVASHDT 47

RESULT 10
Q7VBZ9  Q7VBZ9      PRELIMINARY;      PRT;      546 AA.
AC      Q7VBZ9;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      3,4-dihydroxy-2-butanone 4-phosphate synthase.
DE      Name=ribB; OrderedLocusNames=Pro0943;
OS      Prochlorococcus marinus.
OC      Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC      Prochlorococcus.
OX      NCBI_TaxID=1219;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=SARG / COMP 1375 / SS120;
RX      MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA      Dufréne A., Salanoubat M., Patešny F., Artiguenave F., Axmann I.M.,
RA      Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA      Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA      Scanlan D.J., Tandeau de Marsac N., Weissbach J., Wincker P.,
RA      Wolf Y.I., Hess W.R.;
RT      "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT      a nearly minimal oxypototrophic genome.";
RL      Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025 (2003).

EMBL; AE017163; AAP99987.1; -.
DR      HSSP; O8TG90; 1K49.
DR      GO: GO:0008686; F:3,4 dihydroxy-2-butanone-4-phosphate syntha. . .; IEA.
DR      GO: GO:0003935; F:GTP cyclohydrolase II activity; IEA.
DR      GO: GO:0009231; P:Vitamin B2 biosynthesis; IEA.
DR      InterPro: IPR000422; DHP synthase.
DR      InterPro: IPR000926; GTP CyclohydroII.
DR      Pfam: PF00925; GTP Cyclohydro2; 1.
DR      ProDom: PD003034; DHP synthase; 1.
DR      TIGRFAMS; TIGR00505; ribA; 1.
DR      TIGRFAMS; TIGR00506; ribB; 1.
KW      Complete proteome.
SQ      SEQUENCE 546 AA; 60348 MW; 05453CE83073B5FE CRC64;

Query Match      21.0%; Score 66; DB 2; Length 546;
Best Local Similarity 27.9%; Pred. No. 45;
Matches 17; Conservative 12; Mismatches 24; Indels 8; Gaps 1;

QY      5 RSPVNLPP-----ELRRQSRGSEVNNDSGRYQGLEHGRGSEASPALGKLSDQV 56
Db      382 REPLVNPIDYNYLAIKRTKLGHYIGNDDSGKYVYWKGIYSSNNLSAYKKAQEI 441

QY      57 A 57
Db      442 A 442

RESULT 11
Q9JHT9  Q9JHT9      PRELIMINARY;      PRT;      554 AA.
AC      Q9JHT9;
DT      01-OCT-2000 (TrEMBLrel. 15, Created)
DT      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Guanine nucleotide exchange factor.
DE      Name=Ngef; Synonyms=gef;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=20241931; PubMed=10777665; DOI=10.1006/geno.2000.6138;
RA      Rodrigues N.R., Theodosiou A.M., Nesbit M.A., Campbell L.,
RA      Tandle A.T., Saranath D., Davies K.E.;
RT      "Characterization of Ngef, a novel member of the Dbl family of genes
RT      expressed predominantly in the caudate nucleus.";
RL      Genomics 65:53-61(2000).
CC      -1- SIMILARITY: Contains 1 PH domain.
CC      -1- SIMILARITY: Contains 1 SH3 domain.
DR      EMBL; AJ238898; CAC00698.1; -.
DR      HSSP; O08839; 1BB9.
DR      MGD; MGI:1858414; Ngef.
DR      GO: GO:0008151; P:cell growth and/or maintenance; IDA.
DR      InterPro: IPR011849; PH.
DR      InterPro: IPR011036; PH related.
DR      InterPro: IPR00219; RhoGEF.
DR      InterPro: IPR001452; SH3.
DR      Pfam: PF00169; PH; 1.
DR      Pfam: PF00621; RhoGEF; 1.
DR      Pfam: PF00018; SH3 1; 1.
DR      ProDom: PD000066; SH3; 1.
DR      SMART; SM00233; PH; 1.
DR      SMART; SM00325; RhoGEF; 1.
DR      SMART; SM00326; SH3; 1.
DR      PROSITE; PS0010; DH_2; 1.
DR      PROSITE; PS00003; PH DOMAIN; 1.
DR      PROSITE; PS00002; SH3; 1.
KW      SH3 domain.
SQ      SEQUENCE 554 AA; 64837 MW; 5F3A8FAFBFF5914 CRC64;

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RESULT 14	
Q8TEJ7	
ID	Q8TEJ7 PRELIMINARY; PRT; 677 AA.
AC	Q8TEJ7;
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	FLJ00198 protein (Fragment).
GN	Names=FLJ00198;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_Taxid=9606;

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